

ABSTRACT OF THE DISCLOSURE

The present invention relates to vaccine composition(s) comprising at least two PspAs from strains selected from at least one family, the family being defined by PspAs from strains belonging to the family having greater than or equal to
5 50% homology in aligned sequences of a C-terminal region of an alpha helical region of PspA. Additionally, the families are further comprised of clades, wherein PspAs from strains which belong to a clade exhibit at least 75% sequence homology in aligned sequences of the C-terminal region of the alpha helix of PspA. Vaccine compositions of the present invention preferably comprise a minimum of 4 and a
10 maximum of 6 strains representing a single clade each, and the at least two PspAs are optionally serologically or broadly cross-reactive.